

SEQUENCE LISTING

<110> GARABEDIAN, Michael
 TANEJA, Samir
 HITTELMAN, Adam
 MARKUS, Steven

<120> METHOD FOR SCREENING TRANSCRIPTIONAL COREGULATORY PROTEINS OF TRANSCRIPTION FACTORS, AND ANDROGEN RECEPTOR TRANSCRIPTIONAL COREGULATORY PROTEINS AS TARGETS FOR ANDROGEN RECEPTOR-DEPENDENT DISEASES

<130> GARABEDIAN=1.1A

<140> NOT YET ASSIGNED
 <141> 2001-03-26

<150> 60/225,618
 <151> 2000-08-15

<150> 60/191,768
 <151> 2000-03-24

<160> 20

<170> PatentIn version 3.0

<210> 1
 <211> 474
 <212> DNA
 <213> human

<400> 1
 atggcgacgc cccctaagcg gcgggcggtg gaggccacgg gggagaaaagt gctgcgctac 60
 gagaccttca tcagtgcacgt gctgcagcgg gacttgcgaa aggtgctgga ccatcgagac 120
 aaggatatacg agcagctggc caaatacatt caactgagaa atgtcattga gcgactccag 180
 gaagctaaggc actcggagtt atatatgcag gtggatttgg gctgttaactt cttcggtgac 240
 acagtggtcc cagatacttc acgcatttat gtggccctgg gatatggttt tttcctggag 300
 ttgacactgg cagaagctct caagttcatt gatcgtaaga gctctctcct cacagagctc 360
 agcaacagcc tcaccaagga ctccatgaat atcaaagccc atatccacat gttgcttagag 420
 gggcttagag aactacaagg cctgcagaat ttcccagaga agcctcacca ttga 474

<210> 2
 <211> 157
 <212> PRT
 <213> human

<400> 2

Met Ala Thr Pro Pro Lys Arg Arg Ala Val Glu Ala Thr Gly Glu Lys
 1 5 10 15
 Val Leu Arg Tyr Glu Thr Phe Ile Ser Asp Val Leu Gln Arg Asp Leu
 20 25 30
 Arg Lys Val Leu Asp His Arg Asp Lys Val Tyr Glu Gln Leu Ala Lys

35

40

45

Tyr Leu Gln Leu Arg Asn Val Ile Glu Arg Leu Gln Glu Ala Lys His
 50 55 60

Ser Glu Leu Tyr Met Gln Val Asp Leu Gly Cys Asn Phe Phe Val Asp
 65 70 75 80

Thr Val Val Pro Asp Thr Ser Arg Ile Tyr Val Ala Leu Gly Tyr Gly
 85 90 95

Phe Phe Leu Glu Leu Thr Leu Ala Glu Ala Leu Lys Phe Ile Asp Arg
 100 105 110

Lys Ser Ser Leu Leu Thr Glu Leu Ser Asn Ser Leu Thr Lys Asp Ser
 115 120 125

Met Asn Ile Lys Ala His Ile His Met Leu Leu Glu Gly Leu Arg Glu
 130 135 140

Leu Gln Gly Leu Gln Asn Phe Pro Glu Lys Pro His His
 145 150 155

<210> 3
 <211> 1097
 <212> DNA
 <213> human

<400> 3
 aaatgcacaa cccggacgga agtgcctctc cgacagcaga tccaggctcg gagctccaga 60
 cgctgggaca ggccgcccgc agaccacccc cgccgcgcgc gggacacgac gccccccgca 120
 ggacacgccc atcagcccg aaacctctga gctgcttctc ccggaggccg atgcccaccc 180
 gggagccccc aaagactcgc ggctcccgaa ggcacactgca tactcacccg cctgggcctg 240
 ggcccccgc gcagggactg gcgcggcggag gcctaaaaac cagcgcccccc cgccctccgt 300
 gccagcccca gccgggaccc cacaaggcaa agaccaagaa gattgtgttt gaggatgagt 360
 tgctctccca ggccctcctg ggcgccaaga agcctattgg agccatccct aaggggcata 420
 agcctaggcc ccacccagtg cccgactatg agcttaagta cccgccagtg agcagtgaga 480
 gggAACGGAG ccgctatgtc gcagtgttcc aggaccagta cggagagttc ttggagctcc 540
 agcacgaggt ggggtgtgca caggcaaagc tcaggcagct ggaggccctg ctgagctccc 600
 tgccccacc ccaaagccag aaggaggccc aagttgcagc ccgggtttgg agggagtttg 660
 agatgaagcg aatggatcct ggcttcctgg acaagcaggc tcgctgccac tacctgaagg 720
 gtaaaactgag gcatctcaag actcagatcc agaaattcga tgaccaagga gacagcgagg 780
 gctccgtgta cttctaagtg cccctgcaga tggcagagg gatgcattgg gatgcaggc 840
 cttgcattt cttggtatct ctcagcttt cctttgcag ctccccctac caggggtcgc 900
 tttctcctgg attgcaaatg cctcttcagt ttggactcag ctctgacagc ccctcctcca 960
 ggaaggcatt ccaggacttc ctccctctgg tcctcttagct ctgaccctac agggactcca 1020

gatctcaacc tgccctgg aagttagggcc tgctctccat cccagtgaaa taaacatgt 1080
 ttagacacct aaaaaaa 1097

<210> 4
 <211> 264
 <212> PRT
 <213> Human

<400> 4

Met His Asn Pro Asp Gly Ser Ala Ser Pro Thr Ala Asp Pro Gly Ser
 1 5 10 15

Glu Leu Gln Thr Leu Gly Gln Ala Ala Arg Arg Pro Pro Pro Pro Arg
 20 25 30

Ala Gly His Asp Ala Pro Arg Arg Thr Arg Pro Ser Ala Arg Lys Pro
 35 40 45

Leu Ser Cys Phe Ser Arg Arg Pro Met Pro Thr Arg Glu Pro Pro Lys
 50 55 60

Thr Arg Gly Ser Arg Gly His Leu His Thr His Pro Pro Gly Pro Gly
 65 70 75 80

Pro Pro Leu Gln Gly Leu Ala Pro Arg Gly Leu Lys Thr Ser Ala Pro
 85 90 95

Arg Pro Pro Cys Gln Pro Gln Pro Gly Pro His Lys Ala Lys Thr Lys
 100 105 110

Lys Ile Val Phe Glu Asp Glu Leu Leu Ser Gln Ala Leu Leu Gly Ala
 115 120 125

Lys Lys Pro Ile Gly Ala Ile Pro Lys Gly His Lys Pro Arg Pro His
 130 135 140

Pro Val Pro Asp Tyr Glu Leu Lys Tyr Pro Pro Val Ser Ser Glu Arg
 145 150 155 160

Glu Arg Ser Arg Tyr Val Ala Val Phe Gln Asp Gln Tyr Gly Glu Phe
 165 170 175

Leu Glu Leu Gln His Glu Val Gly Cys Ala Gln Ala Lys Leu Arg Gln
 180 185 190

Leu Glu Ala Leu Leu Ser Ser Leu Pro Pro Pro Gln Ser Gln Lys Glu
 195 200 205

Ala Gln Val Ala Ala Arg Val Trp Arg Glu Phe Glu Met Lys Arg Met
 210 215 220

Asp Pro Gly Phe Leu Asp Lys Gln Ala Arg Cys His Tyr Leu Lys Gly
 225 230 235 240

Lys Leu Arg His Leu Lys Thr Gln Ile Gln Lys Phe Asp Asp Gln Gly
 245 250 255

Asp Ser Glu Gly Ser Val Tyr Phe
 260

<210> 5
<211> 517
<212> DNA
<213> Human

<220>
<221> misc_feature
<223> n at position 65 is unknown.

<400> 5
gaacggcacg agggcgcgccc acgcgcggga agcggcgccgc ggagcgcgcg cggcgccgcg 60
cgccanccgag ggagccgagc gcccgmacgc gcccgcgg acasacgcca gagccgcgcc 120
ccggggccgag cgcaagcgccgc cggccgssygg ggccgcagg ggcgcgccgcg gcggagcg 180
ggcgcgcmga aaaggggccc ggcggagacc aaggcgaggc gcggcccgca agggcgccgg 240
ggaaggcgcc cggcaaggag gcggacaagc ggagcaggcc aacgagacgc gcgcacccac 300
acacgagcgc gagccgcccac aacaccacac ccggcccaag gagaacagca cgccaaacg 360
ccagycacgg cgggcacggg aggccggcca cacacagcgg ccccgccaag gcacggcgca 420
cggcacaagg gcaccacgccc agacaagcga ggagggcagca cgccgagacc ggccggagg 480
ccgcgaccgc cggagaaaag gaacagagag cccccca 517

<210> 6
<211> 189
<212> PRT
<213> Human

<400> 6

Glu Phe Gly Thr Arg Ala Arg Phe Thr Arg Gly Lys Ser Ala Leu Leu
1 5 10 15

Glu Arg Ala Leu Ala Arg Pro Arg Thr Glu Val Ser Leu Ser Ala Phe
20 25 30

Ala Leu Leu Ser Pro Ser Trp Tyr Ser Thr Ala Arg Ala Val Phe Ser
35 40 45

Val Ala Glu Leu Gln Ser Arg Leu Ala Ala Leu Gly Arg Gln Val Gly
50 55 60

Ala Arg Val Leu Asp Ala Leu Val Ala Arg Glu Lys Gly Ala Arg Arg
65 70 75 80

Glu Thr Lys Val Leu Gly Ala Leu Leu Phe Val Lys Gly Ala Val Trp
85 90 95

Lys Ala Leu Phe Gly Lys Glu Ala Asp Lys Leu Glu Gln Ala Asn Asp
100 105 110

Asp Ala Arg Thr Phe Tyr Ile Ile Glu Arg Glu Pro Leu Ile Asn Thr
115 120 125

Tyr Ile Ser Val Pro Lys Glu Asn Ser Thr Leu Asn Cys Ala Ser Phe
130 135 140

Thr Ala Gly Ile Val Glu Ala Val Leu Thr His Ser Gly Phe Pro Ala
 145 150 155 160

Lys Val Thr Ala His Trp His Lys Gly Thr Thr Leu Met Ile Lys Phe
 165 170 175

Glu Glu Ala Val Ile Ala Arg Asp Arg Leu Glu Gly Arg
 180 185

<210> 7
 <211> 126
 <212> DNA
 <213> Human

<400> 7
 gaattcggca cgaggctcaa gccctacgtg agctaacctcg cccctgagag cgaggagacg 60
 cccctgacgg ccgcgcagct cttcagcaag ccgttggcgc cttgccatcg aaaaggactt 120
 caagga 126

<210> 8
 <211> 42
 <212> PRT
 <213> Human

<400> 8

Glu Phe Gly Thr Arg Leu Lys Pro Tyr Val Ser Tyr Leu Ala Pro Glu
 1 5 10 15

Ser Glu Glu Thr Pro Leu Thr Ala Ala Gln Leu Phe Ser Lys Pro Leu
 20 25 30

Ala Pro Cys His Arg Lys Gly Leu Gln Gly
 35 40

<210> 9
 <211> 678
 <212> DNA
 <213> Human

<220>
 <221> misc_feature
 <223> n at position 651 is unknown.

<400> 9
 gaattcggca cgaggattca ttgccccac aatccttaggc ctacccgccc cagtactgat 60
 cattctattt cccctctat tgatccccac ctccaaatat ctcataaca accgactaat 120
 caccacccaa caatgactaa tcaaactaac ctcaaaacaa atgataacca tacacaacac 180
 taaaggacga acctgatctc ttatactagt atccttaatc attttattg ccacaactaa 240
 cctcctcgga ctcctgcctc actcattac accaaccacc caactatcta taaacctagc 300
 catggccatc cccttatgag cgggcgcagt gattataggc ttgcgtcta agattaaaaa 360
 tgccctagcc cacttcttac cacaaggcac acctacaccc cttatcccc tactagttat 420

tatcgaaacc atcagcctac tcattcaacc aataggccctg gccgtacgcc taaccgctaa	480
cattactgca ggccacacct tcatgcaccc aatttggaaagc gccaccctag caatatcaac	540
cattaacctt cctctacact tatcatcttc acaattctaa ttctactgac tattcttagaa	600
atcgctgtcg ccttaatcca agcctacgtt ttccacacttc tagtaaggct ntactgnacg	660
acaacacata aaaaaaaaaa	678

<210> 10
<211> 60
<212> PRT
<213> Human

<400> 10

Glu Phe Gly Thr Arg Ile His Cys Pro His Asn Pro Arg Pro Thr Arg	
1 5 10 15	

Arg Ser Thr Asp His Ser Ile Ser Pro Ser Ile Asp Pro His Leu Gln	
20 25 30	
Ile Ser His Gln Gln Pro Thr Asn His His Pro Thr Met Thr Asn Gln	
35 40 45	

Thr Asn Leu Lys Thr Asn Asp Asn His Thr Gln His	
50 55 60	

<210> 11
<211> 1918
<212> DNA
<213> Human

<400> 11

gaattccaat gtggtaaagt ctgcgtcaa acatcacaac ttgcaaggca ttggagagtt	60
catactggag aaaaaccta caagtgtat gactgtggca gagccttttag tgatcgttca	120
agcctaactt ttcatcaggc aatacatact ggagagaaac cttacaaatg tcatgaatgc	180
ggcaaggttt ttaggcacaa ttcataccctt gcaactcatc ggcgaattca tactggagag	240
aaaccttaca agtgtatga gtgtggaaa gccttagta tgcattcaaa ccttaactacc	300
cataaggta tccatactgg agagaaggct tacaatgtta atcaatgtgg caaggtcttc	360
actcagaact cacacccgtc aaatcatcaa aggactcaca ccggagagaa accttaccga	420
tgcaatgagt gtggaaagc cttcagtgtt cggtcaagcc taaccaccca tcaggcaatc	480
catactggga aaaaaccta caaatgtat gaatgtggca aggtctttac tcaaaatgct	540
cacctggcaa atcaccgaag aattcatact gggagaaac cttacaggtg tacagagtgt	600
gggaaaggct ttagggtaag atcaagtcta actacccata tggcaatcca cactggagaa	660
aagcgttaca aatgtatga gtgtggcaag gtcttcaggc agagttcaaa tcttgcaagt	720
catcacagaa tgcataccgg agagaaacct tacaatgag tgtggtgagg tcattaggtt	780

caattcactc cttcacatc agttaattc attcttgaca gaatccttac aaatgttagt 840
 acagtggcca atccctcatg agttgaagca ttaatagata tgagaggcca taagcaagag 900
 acatcatgt aacatatgtg gcagagggtc tatccaggcc tcgcaggta cttaggcatca 960
 agatttat ctttgatgaa acgaaacaaa tgtaatatgc atcctgaggc cattacccag 1020
 tgaccgatgg taagtgagga ttccttaggag gaataacagt ctctggttc cctgtttgc 1080
 tttgatatta tacactgtag aataactcaca agtccaaata tgctaaaaat tatatattt 1140
 taactcacat acgaaaaggt tgcaggatat ttgttaggcag tcagttacct tcacctttag 1200
 aaatgtttca ctgagttatt tgaggtttt tggaaagcct actattgcgt ttcaatgtga 1260
 actttgaaat cttattgtgc atccttacac accttccatg gtgcttctt ggaaagatca 1320
 ttggatgga aggatcattt attgggtgaa gatcattttagt taggtgaagg attatttcta 1380
 tccaatttgt gaagaaggag gactttgctt taaaattaa gtatcatctg aattagcatt 1440
 tgggagtgcc gaaaaacaat gtaaaactat gatgtcactc accattctga taatgttcag 1500
 ggtgccttcc tcctaccagg agagtactgt ggcttagagg aaagaaatgg tctatcaact 1560
 gaacatgaaa tggagcaggc caagaccta ggacattggg atttttgtgg gaggagagta 1620
 ataggttaatt agacactgat tgtgtggtag aaatactgca gggaaaaagg tcgccccttt 1680
 atgcataaa gagcaatacc tggatgttag caaagagtga tgaaaaattt atcttggttt 1740
 gaaattgaag agagaggcca ggcgcggtgg ctcacacctg taatcccagc actttggag 1800
 gctgaggcag gtggatcacc tgaggtcggg agttcgagac cagcctgacc aacatggaga 1860
 aaccccaatt gtactaaaaa tacaaaatta gccgggcgtg gtggcaggtg cgaaattc 1918

<210> 12
 <211> 252
 <212> PRT
 <213> Human

<400> 12

Glu Phe Gln Cys Gly Lys Val Phe Ala Gln Thr Ser Gln Leu Ala Arg
 1 5 10 15

His Trp Arg Val His Thr Gly Glu Lys Pro Tyr Lys Cys Asn Asp Cys
 20 25 30

Gly Arg Ala Phe Ser Asp Arg Ser Ser Leu Thr Phe His Gln Ala Ile
 35 40 45

His Thr Gly Glu Lys Pro Tyr Lys Cys His Glu Cys Gly Lys Val Phe
 50 55 60

Arg His Asn Ser Tyr Leu Ala Thr His Arg Arg Ile His Thr Gly Glu
 65 70 75 80

Lys Pro Tyr Lys Cys Asn Glu Cys Gly Lys Ala Phe Ser Met His Ser
 85 90 95

Asn Leu Thr Thr His Lys Val Ile His Thr Gly Glu Lys Pro Tyr Lys
 100 105 110

Cys Asn Gln Cys Gly Lys Val Phe Thr Gln Asn Ser His Leu Ala Asn
 115 120 125

His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Arg Cys Asn Glu Cys
 130 135 140

Gly Lys Ala Phe Ser Val Arg Ser Ser Leu Thr Thr His Gln Ala Ile
 145 150 155 160

His Thr Gly Lys Lys Pro Tyr Lys Cys Asn Glu Cys Gly Lys Val Phe
 165 170 175

Thr Gln Asn Ala His Leu Ala Asn His Arg Arg Ile His Thr Gly Glu
 180 185 190

Lys Pro Tyr Arg Cys Thr Glu Cys Gly Lys Ala Phe Arg Val Arg Ser
 195 200 205

Ser Leu Thr Thr His Met Ala Ile His Thr Gly Glu Lys Arg Tyr Lys
 210 215 220

Cys Asn Glu Cys Gly Lys Val Phe Arg Gln Ser Ser Asn Leu Ala Ser
 225 230 235 240

His His Arg Met His Thr Gly Glu Lys Pro Tyr Lys
 245 250

<210> 13

<211> 8588

<212> DNA

<213> Human

<400> 13

cgcggcccgga gcgcctcttt tcgggattaa aagcgccgccc agctcccgcc gccgccccgg 60

tgcggcaggcg cggccgtcgca gcccggcccg ccggagaagc aaccgctggg cggtgagatc 120

cccttagaca tgcggctcggt gggcgcccgat ctgggtgtcag aggagctgtat gaacctgggc 180

gagagcttca tccagaccaa cgaccgtcg ctgaagctct tccagtgcgc cgtctgcaac 240

aagttcacga cggacaacct ggacatgtcg ggcctgcaca tgaacgtgga gcgccgcctg 300

tcgaggacg agtggaaaggc ggtgatgggg gactcataacc agtgcaagct ctggcgctac 360

aacacccagc tcaaggccaa cttccagctg cactgcaaga cagacaagca cgtgcagaag 420

taccagctgg tggcccatcat caaggaggcc ggcaggccca acgagttggag gctcaagtgt 480

gtggccatcg gcaaccccggt gcacctcaag tgcaacgcct gtgactacta caccaacagc 540

ctggagaagc tgcggctcgca cacggtcac tccaggcaccg aggccaggct gaagttgtac 600

aagcacctgc agcagcatga gagtggtgtta gaaggtgaga gctgctacta ccactgcgtt 660

ctgtgcaact actccaccaa ggccaagctc aacctcatcc agcatgtgcg ctccatgaag 720

caccagcgaa gcgagagcct gcgaaagctg cagcggtgc agaaggccct tccagaggag 780

gacgaggacc	tggggcagat	cttcaccatc	cgcagggtgcc	cctccacgga	cccagaagaa	840
gccattgaag	atgttgaagg	accagtcaa	acagctgctg	atccagagga	gcttgctaag	900
gaccaagagg	gcggagcatc	gtccagccaa	gcagagaagg	agctgacaga	ttctcctgca	960
acctccaaac	gcatctcctt	cccaggtagc	tcagagtctc	ccctctcttc	gaagcgacca	1020
aaaacagctg	aggagatcaa	accggagcag	atgtaccagt	gtccctactg	caagtacagt	1080
aatgccgatg	tcaaccggct	ccgggtgcat	gccatgacgc	agcactcggt	gcaacccatg	1140
cttcgctgcc	ccctgtgcca	ggacatgctc	aacaacaaga	tccaccccca	gctgcacctc	1200
acccacctcc	acagcgtggc	acctgactgc	gtggagaagc	tcattatgac	ggtgaccacc	1260
cctgagatgg	tgatgccaag	cagcatgttc	ctcccagcag	ctgttccaga	tcgagatggg	1320
aattccaatt	tggaagaggc	aggaaagcag	cctgaaacct	cagaggatct	gggaaagaac	1380
atcttgccat	ccgcaagcac	agagcaaagc	ggagatttga	aaccatcccc	tgctgaccac	1440
ggctctgtga	gagaagactc	aggcttcata	tgctggaaga	aggggtgcaa	ccaggtttc	1500
aaaacttctg	ctgcccattca	gacgcatttt	aatgaagtgc	atgccaagag	gcctcagctg	1560
ccgggtgtca	atcgccatgt	gtacaagtac	cgctgtaatc	agttagcct	ggccttcaag	1620
accattgaaa	agttgcagct	ccattctcag	taccatgtga	tcagagctgc	caccatgtgc	1680
tgtctttgtc	agcgcagttt	ccgaactttc	caggctctga	agaagcacct	tgagacaagc	1740
cacctggagc	tgagtgaggc	tgacatccaa	cagcttatg	gtggcctgct	ggccaatggg	1800
gacctcctgg	caatgggaga	ccccactctg	gctgaggacc	ataccataat	tgttgaggaa	1860
gacaaggagg	aagagagtga	cttggaaagat	aaacagagcc	caacgggcag	tgactctggg	1920
tcagtacaag	aagactcggg	ctcagagcca	aagagagctc	tgcctttcag	aaaaggtccc	1980
aattttacta	tggaaaagtt	cctagaccct	tctcgccctt	acaagtgtac	cgtctgcaag	2040
gaatctttca	ctcaaaaagaa	tatcctgcta	gtacactaca	attctgtctc	ccacctgcat	2100
aagttaaaga	gagcccttca	agaatcagca	accggtcagc	cagaacccac	cagcagccca	2160
gacaacaaac	cttttaagtg	taacacttgt	aatgtggcct	acagccagag	ttccactctg	2220
gagatccata	tgaggtctgt	gttacatcaa	accaaggccc	gggcagccaa	gctggaggct	2280
gcaagtggca	gcagcaatgg	gactggaaac	agcagcagta	tttccttgag	ctccctccacg	2340
ccaagtccctg	tgagcaccag	tggcagtaac	acctttacca	cctccaaatcc	aagcagtgt	2400
ggcattgctc	caagctctaa	cttactaagc	caagtgcucca	ctgagagtgt	agggatgcca	2460
cccccgggaa	atcctattgg	tgccaaacatt	gcttcccctt	cagagccaa	agaggccat	2520
cggaaagaaac	tggcagatat	gattgcattcc	aggcagcagc	aacaacagca	gcagcaacag	2580
caacaacaac	aacaacaaca	acaacaacaa	gcacaaacgc	tggcccaggc	ccaggctcaa	2640
gttcaagctc	acctgcagca	ggagctgcag	caacaggctg	ccctgatcca	gtctcagctg	2700

ttaacccca	ccctccttcc	tcacttcccc	atgacaactg	agaccctgct	gcaactacag	2760
cagcagcagc	acctccttctt	ccctttctac	atccccagtg	ctgagttcca	gcttaacccc	2820
gaggtgagct	tgccagtgac	cagtggggca	ctgacactga	ctgggacagg	cccaggcctg	2880
ctggaagatc	tgaaggctca	ggttcaggtc	ccacagcaga	gccatcagca	gatcttgccg	2940
cagcagcagc	agaaccaact	ctctatagcc	cagagtact	ctgccttcct	tcagccaagc	3000
cagcaccccg	aaaagaagaa	caaattggtc	atcaaagaaa	aggaaaaaaga	aagccagaga	3060
gagagggaca	gcgcggaggg	gggagagggc	aacaccggtc	cgaaggaaac	actgcccagat	3120
gccttgaagg	ccaaagagaa	gaaagagttg	gcaccagggg	gtggttctga	gccttccatg	3180
ctccctccac	gcattgcttc	agatgccaga	ggAACGCCA	ccaaggccct	gctggagaac	3240
tttggctttg	agttggtcat	ccagtataat	gagaacaagc	agaaggtgca	aaaaaagaat	3300
ggaagactg	accagggaga	gaacctggaa	aagctcgagt	gtgactcctg	cggcaagttg	3360
tttccaaca	tcttgatttt	aaagagtcat	caagagcacf	ttcatcagaa	ttactttctt	3420
ttcaaacagc	tcgagaggtt	tgccaaacag	tacagagacc	actacgataa	actgtaccca	3480
ctgaggcccc	agaccccaga	gccaccacca	cctccccctc	cacccctcc	accccccactt	3540
ccggcagcgc	cgcctcagcc	ggcgtccaca	ccagccatcc	ccgcatcagc	cccacccatc	3600
acctcaccta	caattgcacc	ggcccagcca	tcagtgccgc	tcacccagct	ctccatgccg	3660
atggagctgc	ccatcttctc	gccgctgatg	atgcagacga	tgccgctgca	gaccttgccg	3720
gctcagctac	cccccgagct	gggacctgtg	gagcctctgc	ctgcggacct	ggcccaactc	3780
taccagcatc	agctcaatcc	aaccctgctc	cagcagcaga	acaagaggcc	tcgcaccagg	3840
atcacagatg	atcagctccg	agtcttgccg	caatattttg	acattaacaa	ctcccccagt	3900
gaagagcaaa	taaaagagat	ggcagacaag	tccgggttgc	cccagaaagt	gatcaagcac	3960
tgttcagga	acactcttt	caaagagagg	cagcgtaaca	aggactcccc	ttacaacttc	4020
agtaatcctc	ctatcaccag	cctggaggag	ctcaagattg	actccggcc	cccttcgccc	4080
gaacctccaa	agcaggagta	ctggggaaagc	aagaggtctt	caagaacaag	gtttacggac	4140
taccagctga	gggtcttaca	ggacttcttc	gatgccaatg	cttacccaaa	ggatgatgaa	4200
tttgagcaac	tctctaattt	actgaacctt	ccaacccgag	tgatagtgg	gtggtttcag	4260
aatgcccac	agaaggccag	gaagaattat	gagaatcagg	gagagggcaa	agatggagag	4320
cggcgtgagc	ttacaaaatga	tagatacatt	cgaacaagca	acttgaacta	ccagtgc当地	4380
aaatgttagcc	tggtgtttca	gcgcacatctt	gatctcatca	agcaccagaa	gaagctgtgt	4440
tacaaggatg	aggatgagga	ggggcaggac	gacagccaaa	atgaggattc	catggatgcc	4500
atggaaatcc	tgacgcctac	cagctcatcc	tgcagttaccc	cgatgcctc	acaggcttac	4560

agcgccccag caccatcagc caataataca gcttcctccg ctttcttgca gcttacagcg 4620
 gaggctgagg aactggccac cttcaattca aaaacagagg caggcgatga gaaaccaaag 4680
 ctggcggaaag ctcccagtgc acagccaaac caaacccaag aaaagcaagg acaaccaaag 4740
 ccagagctgc agcagcaaga gcagcccgag cagaagacca acactcccc a cagaagctc 4800
 ccccagctgg tgtccctgcc ttcgttgcca cagcctcctc cacaagcgcc ccctccacag 4860
 tgccccttac cccagtcgag ccccagtctc tccca gctct cccacctgccc cctcaagccc 4920
 ctccacacat caactcctca acagctcgca aacctacctc ctcagcta at cccctaccag 4980
 tgtgaccagt gtaagttggc atttccgtca tttgagcact ggcaggagca tcagcagctc 5040
 cacttcctga gcgcgcagaa ccagttcatc cacccccagt ttttggacag gtcctggat 5100
 atgcctttca tgctcttga tcccagtaac ccactcctgg ccagccagct gctctctggg 5160
 gccatacctc agattccagc aagctcagcc acttctcctt caactccaac ctccacaatg 5220
 aacactctca agaggaagct ggaggaaaaag gccagtgcaa gccctggcga aaacgacagt 5280
 gggacaggag gagaagagcc tcagagagac aagcgttga gaacaaccat cacaccggaa 5340
 caactagaaa ttctctacca gaagtatcta ctggattcca atccgactcg aaagatgtt 5400
 gatcacattg cacacgaggt gggcttgaag aaacgtgtgg tacaagtctg gttcagaac 5460
 acccgagctc gggaaaggaa aggacagttc cggcgtgtag gcccagcgca ggcccacagg 5520
 agatgccctt tttgcagagc gctcttcaaa gccaagactg ctcttgaggc tcataatccgg 5580
 tcccgtcact ggcatgaagc caagagagct ggctacaacc taactctgtc tgcgatgctc 5640
 ttagactgtg atggggact ccagatgaaa ggagatattt ttgacggaac tagttttcc 5700
 cacctacccc caagcagtag tgatggtcag ggtgtccccc tctcacctgt gagtaaaacc 5760
 atggaattgt cacccagaac tcttctaagc ctttcctcca ttaagggtgaa agggattgaa 5820
 gactttgaaa gcccctccat gtcctcagtt aatctaaact ttgaccaa ac taagctggac 5880
 aacgatgact gttcctctgt caacacagca atcacagata ccacaactgg agacgaggc 5940
 aacgcagata acgacagtgc aacggaaata gcaactgaaa ccaaatcctc ttctgcaccc 6000
 aacgaagggt tgaccaa acgc ggccatgatg gcaatgtctg agtataa gaga tcgggttgtca 6060
 tctggctgtg tcagccggc cccgagctt tata gcaagg aatatgacaa tgaaggtaca 6120
 gtggactaca gtgaaacctc aagccttgca gatccctgtc ccccgagtcc tgggtgcgagt 6180
 gatatctgcag gcaatctgg tgacagcggg gatccgttgc ggcagaaacg ttttcgcact 6240
 caaatgacca atctgcagct gaaggcttc aagtcatgct ttaatgacta caggacaccc 6300
 actatgctag aatgtgaggt cctggcaat gacattggac tgccaaagag agtcgttcag 6360
 gtctggttcc agaatgcccggc ggcggaa aagaagtcca agttaagcat ggccaagcat 6420
 ttgggtataa accaaacgag ttatgagggc cccaaaacag agtgcacttt gtgtggcactc 6480

aagtacagcg ctcggctgtc tgtacgtgac cataatcttt cccaacagca tatctccaaa 6540
 gttaaagaca ccatttggaaag ccagctggac aaggagaaaag aataactttga cccagccacc 6600
 gtacgtcagt ttagtggctca acaagagttg gaccggatta aaaaggccaa cgaggtcctt 6660
 ggactggcag ctcagcagca agggatgtt gacaacaccc ctcttcaggc ccttaacctt 6720
 cctacagcat atccagcgct ccagggcatt cctccctgtgt tgctccccc cctcaacagc 6780
 ccctccttgc caggcttac tccatccaac acagctttaa cgtctcctaa gccgaacttg 6840
 atgggtctgc ccagcacaac tgttccttcc cctggcctcc ccacttctgg attaccaaat 6900
 aaaccgtcct cagcgtcgct gagctccccca accccagcac aagccacgat ggcgatggc 6960
 cctcagcaac ccccccagca gcagcagcag cagcagcaac cacaggtgca gcagcctccc 7020
 ccggccgccag cagcccagcc gccacccaca ccacagctcc cactgcaaca gcagcagcaa 7080
 cgcaaggaca aagacagtga gaaagtaaag gagaaggaaa aggacaccaa agggaaaggg 7140
 gaacccctgc ctgtccccaa gaaggagaaa ggagaggccc ccacggcaac tgcagccacg 7200
 atctcagccc cgctgcccac catggagtat gcggtagacc ctgcacagct gcaggccctg 7260
 caggccgcgt tgacttcgga ccccacagca ttgctcacaa gccagttcct tccttacttt 7320
 gtaccaggct ttctccctta ttatgctccc cagatccctg gcgcctgca gagcgggtac 7380
 ctgcagccta tgtatggcat ggaaggctg ttcccctaca gccctgcact gtcgcaggcc 7440
 ctgatggggc tgtccccagg ctccctactg cagcagtacc agcaatacca gcagagtctg 7500
 caggaggcaa tttagcagca gcagcagcaa aaagtgcagc agcagcagcc caaagcaagc 7560
 caaaccaggc tcccccccg ggctccttcc ccagacaaag accctgccaa agaatcccc 7620
 aaaccagaag aacagaaaaaa caccggcgt gaggtgtccc ccctcctgcc gaaaactccc 7680
 gaagagccag aagcagaaaag caaaagtgcg gactccctct acgaccctt cattgttcca 7740
 aagggtcagt acaagtttgt ctgcccgaag tgccaggcgg gcttcagcga cgaggaggca 7800
 gcgaggagcc acctgaagtc cctctgcttc ttccggcagt ctgtggtgaa cctgcaagag 7860
 atggtgcttc acgtccccac cggcggcggc ggcggtggca gtggcggcgg cggcggcgg 7920
 ggcggcggcgg gcggcggcgg cggcggcggc tcgttaccact gcctggcgtg cgagagcgcg 7980
 ctctgtgggg aggaagctct gagtcaacat ctcgagtcgg cttgcacaa acacagaaca 8040
 atcacgagag cagcaagaaa cgccaaagag caccctagtt tattacctca ctctgcctgc 8100
 ttccccgatc ctagcaccgc atctacctcg cagtcgtccg ctcactcaa cgacagcccc 8160
 cctcccccgt cggccgcccgc cccctcctcc gcttccccc acgcctccag gaagtcttg 8220
 ccgcaagtgg tctcccgggc ttccggcagcg aagcccccatt ctttcctcc tctctcctca 8280
 tcttcaacgg ttacctcaag ttcatgcagc acctcagggg ttccagccctc gatgccaaca 8340

gacgactatt cgaggaggagtc tgacacggat ctcagccaaa agtccgacgg accggcgagc 8400
 ccggtgagg gtcccaaaga ccccagctgc cccaaggaca gtggtctgac cagtgttagga 8460
 acggacacct tcagattgta agcttgaag atgaacaata caaacaaatg aatttaata 8520
 caaaaattaa taacaaacca atttcaaaaa tagactaact gcaattccaa agcttctaac 8580
 caaaaaac 8588

<210> 14
 <211> 2783
 <212> PRT
 <213> Human

<400> 14

Met	Arg	Leu	Gly	Gly	Gly	Gln	Leu	Val	Ser	Glu	Glu	Leu	Met	Asn	Leu	
1						5			10				15			
Gly	Glu	Ser	Phe	Ile	Gln	Thr	Asn	Asp	Pro	Ser	Leu	Lys	Leu	Phe	Gln	
			20				25					30				
Cys	Ala	Val	Cys	Asn	Lys	Phe	Thr	Thr	Asp	Asn	Leu	Asp	Met	Leu	Gly	
			35			40					45					
Leu	His	Met	Asn	Val	Glu	Arg	Ser	Leu	Ser	Glu	Asp	Glu	Trp	Lys	Ala	
			50			55				60						
Val	Met	Gly	Asp	Ser	Tyr	Gln	Cys	Lys	Leu	Cys	Arg	Tyr	Asn	Thr	Gln	
	65				70				75			80				
Leu	Lys	Ala	Asn	Phe	Gln	Leu	His	Cys	Lys	Thr	Asp	Lys	His	Val	Gln	
				85				90				95				
Lys	Tyr	Gln	Leu	Val	Ala	His	Ile	Lys	Glu	Gly	Gly	Lys	Ala	Asn	Glu	
			100				105					110				
Trp	Arg	Leu	Lys	Cys	Val	Ala	Ile	Gly	Asn	Pro	Val	His	Leu	Lys	Cys	
			115				120				125					
Asn	Ala	Cys	Asp	Tyr	Tyr	Thr	Asn	Ser	Leu	Glu	Lys	Leu	Arg	Leu	His	
			130				135				140					
Thr	Val	Asn	Ser	Arg	His	Glu	Ala	Ser	Leu	Lys	Leu	Tyr	Lys	His	Leu	
	145				150				155				160			
Gln	Gln	His	Glu	Ser	Gly	Val	Glu	Gly	Glu	Ser	Cys	Tyr	Tyr	His	Cys	
			165				170				175					
Val	Leu	Cys	Asn	Tyr	Ser	Thr	Lys	Ala	Lys	Leu	Asn	Leu	Ile	Gln	His	
	180					185					190					
Val	Arg	Ser	Met	Lys	His	Gln	Arg	Ser	Glu	Ser	Leu	Arg	Lys	Leu	Gln	
			195				200				205					
Arg	Leu	Gln	Lys	Gly	Leu	Pro	Glu	Glu	Asp	Asp	Leu	Gly	Gln	Ile		
			210			215				220						
Phe	Thr	Ile	Arg	Arg	Cys	Pro	Ser	Thr	Asp	Pro	Glu	Glu	Ala	Ile	Glu	
	225				230				235				240			

Asp Val Glu Gly Pro Ser Glu Thr Ala Ala Asp Pro Glu Glu Leu Ala
 245 250 255

Lys Asp Gln Glu Gly Gly Ala Ser Ser Ser Gln Ala Glu Lys Glu Leu
 260 265 270

Thr Asp Ser Pro Ala Thr Ser Lys Arg Ile Ser Phe Pro Gly Ser Ser
 275 280 285

Glu Ser Pro Leu Ser Ser Lys Arg Pro Lys Thr Ala Glu Glu Ile Lys
 290 295 300

Pro Glu Gln Met Tyr Gln Cys Pro Tyr Cys Lys Tyr Ser Asn Ala Asp
 305 310 315 320

Val Asn Arg Leu Arg Val His Ala Met Thr Gln His Ser Val Gln Pro
 325 330 335

Met Leu Arg Cys Pro Leu Cys Gln Asp Met Leu Asn Asn Lys Ile His
 340 345 350

Leu Gln Leu His Leu Thr His Leu His Ser Val Ala Pro Asp Cys Val
 355 360 365

Glu Lys Leu Ile Met Thr Val Thr Pro Glu Met Val Met Pro Ser
 370 375 380

Ser Met Phe Leu Pro Ala Ala Val Pro Asp Arg Asp Gly Asn Ser Asn
 385 390 395 400

Leu Glu Glu Ala Gly Lys Gln Pro Glu Thr Ser Glu Asp Leu Gly Lys
 405 410 415

Asn Ile Leu Pro Ser Ala Ser Thr Glu Gln Ser Gly Asp Leu Lys Pro
 420 425 430

Ser Pro Ala Asp Pro Gly Ser Val Arg Glu Asp Ser Gly Phe Ile Cys
 435 440 445

Trp Lys Lys Gly Cys Asn Gln Val Phe Lys Thr Ser Ala Ala Leu Gln
 450 455 460

Thr His Phe Asn Glu Val His Ala Lys Arg Pro Gln Leu Pro Val Ser
 465 470 475 480

Asp Arg His Val Tyr Lys Tyr Arg Cys Asn Gln Cys Ser Leu Ala Phe
 485 490 495

Lys Thr Ile Glu Lys Leu Gln Leu His Ser Gln Tyr His Val Ile Arg
 500 505 510

Ala Ala Thr Met Cys Cys Leu Cys Gln Arg Ser Phe Arg Thr Phe Gln
 515 520 525

Ala Leu Lys Lys His Leu Glu Thr Ser His Leu Glu Leu Ser Glu Ala
 530 535 540

Asp Ile Gln Gln Leu Tyr Gly Gly Leu Leu Ala Asn Gly Asp Leu Leu
 545 550 555 560

Ala Met Gly Asp Pro Thr Leu Ala Glu Asp His Thr Ile Ile Val Glu
 565 570 575

Glu Asp Lys Glu Glu Glu Ser Asp Leu Glu Asp Lys Gln Ser Pro Thr
 580 585 590
 Gly Ser Asp Ser Gly Ser Val Gln Glu Asp Ser Gly Ser Glu Pro Lys
 595 600 605
 Arg Ala Leu Pro Phe Arg Lys Gly Pro Asn Phe Thr Met Glu Lys Phe
 610 615 620
 Leu Asp Pro Ser Arg Pro Tyr Lys Cys Thr Val Cys Lys Glu Ser Phe
 625 630 635 640
 Thr Gln Lys Asn Ile Leu Leu Val His Tyr Asn Ser Val Ser His Leu
 645 650 655
 His Lys Leu Lys Arg Ala Leu Gln Glu Ser Ala Thr Gly Gln Pro Glu
 660 665 670
 Pro Thr Ser Ser Pro Asp Asn Lys Pro Phe Lys Cys Asn Thr Cys Asn
 675 680 685
 Val Ala Tyr Ser Gln Ser Ser Thr Leu Glu Ile His Met Arg Ser Val
 690 695 700
 Leu His Gln Thr Lys Ala Arg Ala Ala Lys Leu Glu Ala Ala Ser Gly
 705 710 715 720
 Ser Ser Asn Gly Thr Gly Asn Ser Ser Ser Ile Ser Leu Ser Ser Ser
 725 730 735
 Thr Pro Ser Pro Val Ser Thr Ser Gly Ser Asn Thr Phe Thr Thr Ser
 740 745 750
 Asn Pro Ser Ser Ala Gly Ile Ala Pro Ser Ser Asn Leu Leu Ser Gln
 755 760 765
 Val Pro Thr Glu Ser Val Gly Met Pro Pro Leu Gly Asn Pro Ile Gly
 770 775 780
 Ala Asn Ile Ala Ser Pro Ser Glu Pro Lys Glu Ala Asn Arg Lys Lys
 785 790 795 800
 Leu Ala Asp Met Ile Ala Ser Arg Gln Gln Gln Gln Gln Gln Gln
 805 810 815
 Gln Gln Gln Gln Gln Gln Gln Gln Gln Ala Gln Thr Leu Ala
 820 825 830
 Gln Ala Gln Ala Gln Val Gln Ala His Leu Gln Gln Glu Leu Gln Gln
 835 840 845
 Gln Ala Ala Leu Ile Gln Ser Gln Leu Phe Asn Pro Thr Leu Leu Pro
 850 855 860
 His Phe Pro Met Thr Thr Glu Thr Leu Leu Gln Leu Gln Gln Gln Gln
 865 870 875 880
 His Leu Leu Phe Pro Phe Tyr Ile Pro Ser Ala Glu Phe Gln Leu Asn
 885 890 895
 Pro Glu Val Ser Leu Pro Val Thr Ser Gly Ala Leu Thr Leu Thr Gly
 900 905 910

Thr Gly Pro Gly Leu Leu Glu Asp Leu Lys Ala Gln Val Gln Val Pro
 915 920 925
 Gln Gln Ser His Gln Gln Ile Leu Pro Gln Gln Gln Asn Gln Leu
 930 935 940
 Ser Ile Ala Gln Ser His Ser Ala Leu Leu Gln Pro Ser Gln His Pro
 945 950 955 960
 Glu Lys Lys Asn Lys Leu Val Ile Lys Glu Lys Glu Lys Glu Ser Gln
 965 970 975
 Arg Glu Arg Asp Ser Ala Glu Gly Gly Glu Gly Asn Thr Gly Pro Lys
 980 985 990
 Glu Thr Leu Pro Asp Ala Leu Lys Ala Lys Glu Lys Lys Glu Leu Ala
 995 1000 1005
 Pro Gly Gly Ser Glu Pro Ser Met Leu Pro Pro Arg Ile Ala
 1010 1015 1020
 Ser Asp Ala Arg Gly Asn Ala Thr Lys Ala Leu Leu Glu Asn Phe
 1025 1030 1035
 Gly Phe Glu Leu Val Ile Gln Tyr Asn Glu Asn Lys Gln Lys Val
 1040 1045 1050
 Gln Lys Lys Asn Gly Lys Thr Asp Gln Gly Glu Asn Leu Glu Lys
 1055 1060 1065
 Leu Glu Cys Asp Ser Cys Gly Lys Leu Phe Ser Asn Ile Leu Ile
 1070 1075 1080
 Leu Lys Ser His Gln Glu His Val His Gln Asn Tyr Phe Pro Phe
 1085 1090 1095
 Lys Gln Leu Glu Arg Phe Ala Lys Gln Tyr Arg Asp His Tyr Asp
 1100 1105 1110
 Lys Leu Tyr Pro Leu Arg Pro Gln Thr Pro Glu Pro Pro Pro Pro
 1115 1120 1125
 Pro Pro Pro Pro Pro Pro Leu Pro Ala Ala Pro Pro Gln
 1130 1135 1140
 Pro Ala Ser Thr Pro Ala Ile Pro Ala Ser Ala Pro Pro Ile Thr
 1145 1150 1155
 Ser Pro Thr Ile Ala Pro Ala Gln Pro Ser Val Pro Leu Thr Gln
 1160 1165 1170
 Leu Ser Met Pro Met Glu Leu Pro Ile Phe Ser Pro Leu Met Met
 1175 1180 1185
 Gln Thr Met Pro Leu Gln Thr Leu Pro Ala Gln Leu Pro Pro Gln
 1190 1195 1200
 Leu Gly Pro Val Glu Pro Leu Pro Ala Asp Leu Ala Gln Leu Tyr
 1205 1210 1215
 Gln His Gln Leu Asn Pro Thr Leu Leu Gln Gln Gln Asn Lys Arg
 1220 1225 1230

Pro Arg Thr Arg Ile Thr Asp Asp Gln Leu Arg Val Leu Arg Gln
 1235 1240 1245
 Tyr Phe Asp Ile Asn Asn Ser Pro Ser Glu Glu Gln Ile Lys Glu
 1250 1255 1260
 Met Ala Asp Lys Ser Gly Leu Pro Gln Lys Val Ile Lys His Trp
 1265 1270 1275
 Phe Arg Asn Thr Leu Phe Lys Glu Arg Gln Arg Asn Lys Asp Ser
 1280 1285 1290
 Pro Tyr Asn Phe Ser Asn Pro Pro Ile Thr Ser Leu Glu Glu Leu
 1295 1300 1305
 Lys Ile Asp Ser Arg Pro Pro Ser Pro Glu Pro Pro Lys Gln Glu
 1310 1315 1320
 Tyr Trp Gly Ser Lys Arg Ser Ser Arg Thr Arg Phe Thr Asp Tyr
 1325 1330 1335
 Gln Leu Arg Val Leu Gln Asp Phe Phe Asp Ala Asn Ala Tyr Pro
 1340 1345 1350
 Lys Asp Asp Glu Phe Glu Gln Leu Ser Asn Leu Leu Asn Leu Pro
 1355 1360 1365
 Thr Arg Val Ile Val Val Trp Phe Gln Asn Ala Arg Gln Lys Ala
 1370 1375 1380
 Arg Lys Asn Tyr Glu Asn Gln Gly Glu Gly Lys Asp Gly Glu Arg
 1385 1390 1395
 Arg Glu Leu Thr Asn Asp Arg Tyr Ile Arg Thr Ser Asn Leu Asn
 1400 1405 1410
 Tyr Gln Cys Lys Lys Cys Ser Leu Val Phe Gln Arg Ile Phe Asp
 1415 1420 1425
 Leu Ile Lys His Gln Lys Lys Leu Cys Tyr Lys Asp Glu Asp Glu
 1430 1435 1440
 Glu Gly Gln Asp Asp Ser Gln Asn Glu Asp Ser Met Asp Ala Met
 1445 1450 1455
 Glu Ile Leu Thr Pro Thr Ser Ser Ser Cys Ser Thr Pro Met Pro
 1460 1465 1470
 Ser Gln Ala Tyr Ser Ala Pro Ala Pro Ser Ala Asn Asn Thr Ala
 1475 1480 1485
 Ser Ser Ala Phe Leu Gln Leu Thr Ala Glu Ala Glu Glu Leu Ala
 1490 1495 1500
 Thr Phe Asn Ser Lys Thr Glu Ala Gly Asp Glu Lys Pro Lys Leu
 1505 1510 1515
 Ala Glu Ala Pro Ser Ala Gln Pro Asn Gln Thr Gln Glu Lys Gln
 1520 1525 1530
 Gly Gln Pro Lys Pro Glu Leu Gln Gln Gln Glu Gln Pro Glu Gln
 1535 1540 1545

Lys Thr Asn Thr Pro Gln Gln Lys Leu Pro Gln Leu Val Ser Leu
 1550 1555 1560
 Pro Ser Leu Pro Gln Pro Pro Pro Gln Ala Pro Pro Pro Gln Cys
 1565 1570 1575
 Pro Leu Pro Gln Ser Ser Pro Ser Pro Ser Gln Leu Ser His Leu
 1580 1585 1590
 Pro Leu Lys Pro Leu His Thr Ser Thr Pro Gln Gln Leu Ala Asn
 1595 1600 1605
 Leu Pro Pro Gln Leu Ile Pro Tyr Gln Cys Asp Gln Cys Lys Leu
 1610 1615 1620
 Ala Phe Pro Ser Phe Glu His Trp Gln Glu His Gln Gln Leu His
 1625 1630 1635
 Phe Leu Ser Ala Gln Asn Gln Phe Ile His Pro Gln Phe Leu Asp
 1640 1645 1650
 Arg Ser Leu Asp Met Pro Phe Met Leu Phe Asp Pro Ser Asn Pro
 1655 1660 1665
 Leu Leu Ala Ser Gln Leu Leu Ser Gly Ala Ile Pro Gln Ile Pro
 1670 1675 1680
 Ala Ser Ser Ala Thr Ser Pro Ser Thr Pro Thr Ser Thr Met Asn
 1685 1690 1695
 Thr Leu Lys Arg Lys Leu Glu Glu Lys Ala Ser Ala Ser Pro Gly
 1700 1705 1710
 Glu Asn Asp Ser Gly Thr Gly Gly Glu Glu Pro Gln Arg Asp Lys
 1715 1720 1725
 Arg Leu Arg Thr Thr Ile Thr Pro Glu Gln Leu Glu Ile Leu Tyr
 1730 1735 1740
 Gln Lys Tyr Leu Leu Asp Ser Asn Pro Thr Arg Lys Met Leu Asp
 1745 1750 1755
 His Ile Ala His Glu Val Gly Leu Lys Lys Arg Val Val Gln Val
 1760 1765 1770
 Trp Phe Gln Asn Thr Arg Ala Arg Glu Arg Lys Gly Gln Phe Arg
 1775 1780 1785
 Ala Val Gly Pro Ala Gln Ala His Arg Arg Cys Pro Phe Cys Arg
 1790 1795 1800
 Ala Leu Phe Lys Ala Lys Thr Ala Leu Glu Ala His Ile Arg Ser
 1805 1810 1815
 Arg His Trp His Glu Ala Lys Arg Ala Gly Tyr Asn Leu Thr Leu
 1820 1825 1830
 Ser Ala Met Leu Leu Asp Cys Asp Gly Gly Leu Gln Met Lys Gly
 1835 1840 1845
 Asp Ile Phe Asp Gly Thr Ser Phe Ser His Leu Pro Pro Ser Ser
 1850 1855 1860

Ser Asp Gly Gln Gly Val Pro Leu Ser Pro Val Ser Lys Thr Met
 1865 1870 1875
 Glu Leu Ser Pro Arg Thr Leu Leu Ser Pro Ser Ser Ile Lys Val
 1880 1885 1890
 Glu Gly Ile Glu Asp Phe Glu Ser Pro Ser Met Ser Ser Val Asn
 1895 1900 1905
 Leu Asn Phe Asp Gln Thr Lys Leu Asp Asn Asp Asp Cys Ser Ser
 1910 1915 1920
 Val Asn Thr Ala Ile Thr Asp Thr Thr Thr Gly Asp Glu Gly Asn
 1925 1930 1935
 Ala Asp Asn Asp Ser Ala Thr Gly Ile Ala Thr Glu Thr Lys Ser
 1940 1945 1950
 Ser Ser Ala Pro Asn Glu Gly Leu Thr Lys Ala Ala Met Met Ala
 1955 1960 1965
 Met Ser Glu Tyr Glu Asp Arg Leu Ser Ser Gly Leu Val Ser Pro
 1970 1975 1980
 Ala Pro Ser Phe Tyr Ser Lys Glu Tyr Asp Asn Glu Gly Thr Val
 1985 1990 1995
 Asp Tyr Ser Glu Thr Ser Ser Leu Ala Asp Pro Cys Ser Pro Ser
 2000 2005 2010
 Pro Gly Ala Ser Gly Ser Ala Gly Lys Ser Gly Asp Ser Gly Asp
 2015 2020 2025
 Arg Pro Gly Gln Lys Arg Phe Arg Thr Gln Met Thr Asn Leu Gln
 2030 2035 2040
 Leu Lys Val Leu Lys Ser Cys Phe Asn Asp Tyr Arg Thr Pro Thr
 2045 2050 2055
 Met Leu Glu Cys Glu Val Leu Gly Asn Asp Ile Gly Leu Pro Lys
 2060 2065 2070
 Arg Val Val Gln Val Trp Phe Gln Asn Ala Arg Ala Lys Glu Lys
 2075 2080 2085
 Lys Ser Lys Leu Ser Met Ala Lys His Phe Gly Ile Asn Gln Thr
 2090 2095 2100
 Ser Tyr Glu Gly Pro Lys Thr Glu Cys Thr Leu Cys Gly Ile Lys
 2105 2110 2115
 Tyr Ser Ala Arg Leu Ser Val Arg Asp His Ile Phe Ser Gln Gln
 2120 2125 2130
 His Ile Ser Lys Val Lys Asp Thr Ile Gly Ser Gln Leu Asp Lys
 2135 2140 2145
 Glu Lys Glu Tyr Phe Asp Pro Ala Thr Val Arg Gln Leu Met Ala
 2150 2155 2160
 Gln Gln Glu Leu Asp Arg Ile Lys Lys Ala Asn Glu Val Leu Gly
 2165 2170 2175

Leu Ala Ala Gln Gln Gln Gly Met Phe Asp Asn Thr Pro Leu Gln
 2180 2185 2190
 Ala Leu Asn Leu Pro Thr Ala Tyr Pro Ala Leu Gln Gly Ile Pro
 2195 2200 2205
 Pro Val Leu Leu Pro Gly Leu Asn Ser Pro Ser Leu Pro Gly Phe
 2210 2215 2220
 Thr Pro Ser Asn Thr Ala Leu Thr Ser Pro Lys Pro Asn Leu Met
 2225 2230 2235
 Gly Leu Pro Ser Thr Thr Val Pro Ser Pro Gly Leu Pro Thr Ser
 2240 2245 2250
 Gly Leu Pro Asn Lys Pro Ser Ser Ala Ser Leu Ser Ser Pro Thr
 2255 2260 2265
 Pro Ala Gln Ala Thr Met Ala Met Gly Pro Gln Gln Pro Pro Gln
 2270 2275 2280
 Gln Gln Gln Gln Gln Gln Pro Gln Val Gln Gln Pro Pro Pro
 2285 2290 2295
 Pro Pro Ala Ala Gln Pro Pro Pro Thr Pro Gln Leu Pro Leu Gln
 2300 2305 2310
 Gln Gln Gln Gln Arg Lys Asp Lys Asp Ser Glu Lys Val Lys Glu
 2315 2320 2325
 Lys Glu Lys Ala His Lys Gly Lys Gly Glu Pro Leu Pro Val Pro
 2330 2335 2340
 Lys Lys Glu Lys Gly Glu Ala Pro Thr Ala Thr Ala Ala Thr Ile
 2345 2350 2355
 Ser Ala Pro Leu Pro Thr Met Glu Tyr Ala Val Asp Pro Ala Gln
 2360 2365 2370
 Leu Gln Ala Leu Gln Ala Ala Leu Thr Ser Asp Pro Thr Ala Leu
 2375 2380 2385
 Leu Thr Ser Gln Phe Leu Pro Tyr Phe Val Pro Gly Phe Ser Pro
 2390 2395 2400
 Tyr Tyr Ala Pro Gln Ile Pro Gly Ala Leu Gln Ser Gly Tyr Leu
 2405 2410 2415
 Gln Pro Met Tyr Gly Met Glu Gly Leu Phe Pro Tyr Ser Pro Ala
 2420 2425 2430
 Leu Ser Gln Ala Leu Met Gly Leu Ser Pro Gly Ser Leu Leu Gln
 2435 2440 2445
 Gln Tyr Gln Gln Tyr Gln Gln Ser Leu Gln Glu Ala Ile Gln Gln
 2450 2455 2460
 Gln Gln Gln Gln Lys Val Gln Gln Gln Gln Pro Lys Ala Ser Gln
 2465 2470 2475
 Thr Pro Val Pro Pro Gly Ala Pro Ser Pro Asp Lys Asp Pro Ala
 2480 2485 2490

Lys Glu Ser Pro Lys Pro Glu Glu Gln Lys Asn Thr Pro Arg Glu
 2495 2500 2505
 Val Ser Pro Leu Leu Pro Lys Leu Pro Glu Glu Pro Glu Ala Glu
 2510 2515 2520
 Ser Lys Ser Ala Asp Ser Leu Tyr Asp Pro Phe Ile Val Pro Lys
 2525 2530 2535
 Val Gln Tyr Lys Leu Val Cys Arg Lys Cys Gln Ala Gly Phe Ser
 2540 2545 2550
 Asp Glu Glu Ala Ala Arg Ser His Leu Lys Ser Leu Cys Phe Phe
 2555 2560 2565
 Gly Gln Ser Val Val Asn Leu Gln Glu Met Val Leu His Val Pro
 2570 2575 2580
 Thr Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Gly Gly Gly
 2585 2590 2595
 Gly Gly Gly Gly Gly Gly Gly Gly Ser Tyr His Cys Leu Ala
 2600 2605 2610
 Cys Glu Ser Ala Leu Cys Gly Glu Glu Ala Leu Ser Gln His Leu
 2615 2620 2625
 Glu Ser Ala Leu His Lys His Arg Thr Ile Thr Arg Ala Ala Arg
 2630 2635 2640
 Asn Ala Lys Glu His Pro Ser Leu Leu Pro His Ser Ala Cys Phe
 2645 2650 2655
 Pro Asp Pro Ser Thr Ala Ser Thr Ser Gln Ser Ala Ala His Ser
 2660 2665 2670
 Asn Asp Ser Pro Pro Pro Pro Ser Ala Ala Ala Pro Ser Ser Ala
 2675 2680 2685
 Ser Pro His Ala Ser Arg Lys Ser Trp Pro Gln Val Val Ser Arg
 2690 2695 2700
 Ala Ser Ala Ala Lys Pro Pro Ser Phe Pro Pro Leu Ser Ser Ser
 2705 2710 2715
 Ser Thr Val Thr Ser Ser Ser Cys Ser Thr Ser Gly Val Gln Pro
 2720 2725 2730
 Ser Met Pro Thr Asp Asp Tyr Ser Glu Glu Ser Asp Thr Asp Leu
 2735 2740 2745
 Ser Gln Lys Ser Asp Gly Pro Ala Ser Pro Val Glu Gly Pro Lys
 2750 2755 2760
 Asp Pro Ser Cys Pro Lys Asp Ser Gly Leu Thr Ser Val Gly Thr
 2765 2770 2775
 Asp Thr Phe Arg Leu
 2780

<210> 15
 <211> 30
 <212> DNA

<213> Artificial	
<220>	
<223> synthetic	
<400> 15	
agatcttaag cagaaatgtat tgcaccattg	30
<210> 16	
<211> 28	
<212> DNA	
<213> Artificial	
<220>	
<223> synthetic	
<400> 16	
gttagataaaag gtgtgtgtca ctgagctc	28
<210> 17	
<211> 19	
<212> DNA	
<213> Artificial	
<220>	
<223> synthetic	
<400> 17	
ttggggtttat tcgcaacgg	19
<210> 18	
<211> 35	
<212> DNA	
<213> Artificial	
<220>	
<223> synthetic	
<400> 18	
gaactggatc cctgctcata tactttgtct cgatg	35
<210> 19	
<211> 26	
<212> DNA	
<213> Artificial	
<220>	
<223> synthetic	
<400> 19	
gaactggatc caccaaggac tccatg	26
<210> 20	
<211> 18	
<212> DNA	
<213> Artificial	
<220>	

<223> synthetic

<400> 20

cggaaattagc ttggctgc

18